



# results of BLAST

**BLASTN 2.2.12 [Aug-07-2005]**

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1126736645-6349-116079271193.BLASTQ1

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)  
3,491,285 sequences; 15,298,534,039 total letters

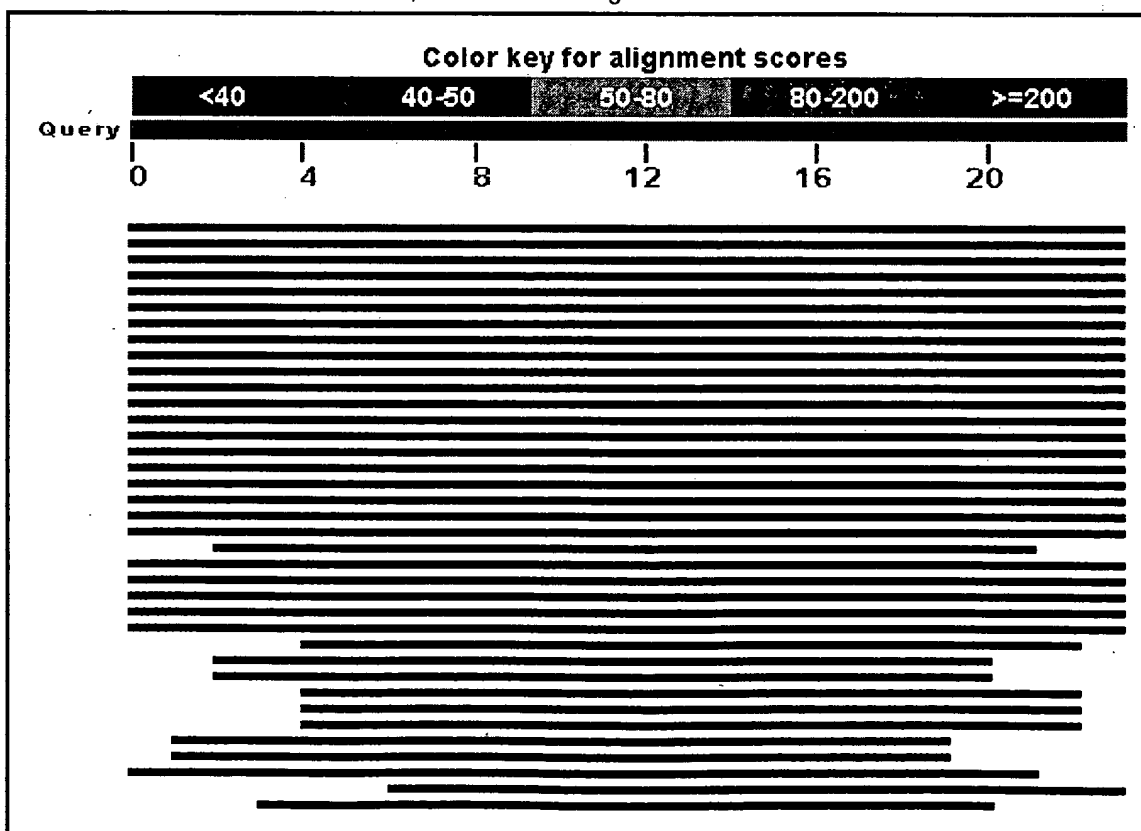
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)  
[Taxonomy reports](#)

**Query=**

(23 letters)

## Distribution of 48 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



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Sequences producing significant alignments:			Score (Bits)	E Value	
<a href="#">gi 55645360 ref XM_511474.1 </a>	PREDICTED: Pan troglodytes DNA t...		46.1	0.001	G
<a href="#">gi 19913405 ref NM_001067.2 </a>	Homo sapiens topoisomerase (DNA) II		46.1	0.001	U
<a href="#">gi 15488575 gb BC013429.1 </a>	Homo sapiens topoisomerase (DNA) I...		46.1	0.001	U
<a href="#">gi 292829 gb J04088.1 HUMTOPII</a>	Human DNA topoisomerase II (top2)		46.1	0.001	U
<a href="#">gi 19913407 ref NM_001068.2 </a>	Homo sapiens topoisomerase (DNA) II		38.2	0.25	U
<a href="#">gi 73990501 ref XM_534241.2 </a>	PREDICTED: Canis familiaris simi...		38.2	0.25	G
<a href="#">gi 73966010 ref XM_857989.1 </a>	PREDICTED: Canis familiaris simi...		38.2	0.25	G
<a href="#">gi 73966008 ref XM_537646.2 </a>	PREDICTED: Canis familiaris simi...		38.2	0.25	G
<a href="#">gi 55619958 ref XM_516332.1 </a>	PREDICTED: Pan troglodytes DNA t...		38.2	0.25	G
<a href="#">gi 45382160 ref NM_204791.1 </a>	Gallus gallus topoisomerase (DNA) I		38.2	0.25	U
<a href="#">gi 587514 emb Z46372.1 RNDNATI2</a>	R.norvegicus RNA for DNA topoiso		38.2	0.25	E
<a href="#">gi 57963 emb Z19552.1 RNDNATPII</a>	R.norvegicus mRNA for DNA topoiso		38.2	0.25	U
<a href="#">gi 2909392 emb Y16595.1 CLTOPO4</a>	Cricetulus longicaudatus mRNA...		38.2	0.25	
<a href="#">gi 2909390 emb Y16594.1 CLTOPO3</a>	Cricetulus longicaudatus mRNA...		38.2	0.25	
<a href="#">gi 37230 emb X68060.1 HSTOPIIB</a>	H.sapiens topIIB mRNA for topoiso		38.2	0.25	U
<a href="#">gi 55725809 emb CR857392.1 </a>	Pongo pygmaeus mRNA; cDNA DKFZp46...		38.2	0.25	
<a href="#">gi 62087337 dbj AB208879.1 </a>	Homo sapiens mRNA for DNA topoiso...		38.2	0.25	G
<a href="#">gi 38259191 ref NM_022183.2 </a>	Rattus norvegicus topoisomerase (DN		38.2	0.25	U
<a href="#">gi 6755848 ref NM_011623.1 </a>	Mus musculus topoisomerase (DNA) II		38.2	0.25	U
<a href="#">gi 10121856 gb AF285155.1 AF285155</a>	Gallus gallus topoisomeras...		38.2	0.25	U
<a href="#">gi 27452890 gb AC137053.2 </a>	Homo sapiens 12 BAC RP11-64103 (Ro...		38.2	0.25	
<a href="#">gi 54400871 gb AC122444.4 </a>	Mus musculus BAC clone RP24-23219 fro		38.2	0.25	
<a href="#">gi 6714552 dbj AB007445.2 </a>	Gallus gallus mRNA for DNA topoisomer		38.2	0.25	U
<a href="#">gi 220615 dbj D12513.1 MUSTOP2</a>	Mouse mRNA for DNA topoisomerase		38.2	0.25	U
<a href="#">gi 339809 gb M27504.1 HUMTOPIIX</a>	Homo sapiens topoisomerase type		38.2	0.25	U
<a href="#">gi 191217 gb L04607.1 CRUTOPISII</a>	Cricetulus griseus DNA topoisom		38.2	0.25	
<a href="#">gi 50911806 ref XM_467311.1 </a>	Oryza sativa (japonica cultivar-gro		36.2	0.98	G
<a href="#">gi 33457259 gb AC125538.4 </a>	Mus musculus BAC clone RP24-178B2 ...		36.2	0.98	
<a href="#">gi 19909460 gb AC098708.3 </a>	Mus musculus BAC clone RP23-1116 from		36.2	0.98	
<a href="#">gi 58530788 dbj AP008208.1 </a>	Oryza sativa (japonica cultivar-g...		36.2	0.98	
<a href="#">gi 41052945 dbj AP004778.3 </a>	Oryza sativa (japonica cultivar-g...		36.2	0.98	
<a href="#">gi 32982494 dbj AK072471.1 </a>	Oryza sativa (japonica cultivar-g...		36.2	0.98	U
<a href="#">gi 57226287 gb AE017344.1 </a>	Cryptococcus neoformans var. neofo...		36.2	0.98	
<a href="#">gi 58266227 ref XM_570270.1 </a>	Filobasidiella neoformans expres...		36.2	0.98	G
<a href="#">gi 32399348 emb BX546470.1 </a>	Human DNA sequence from clone WI2...		34.2	3.9	
<a href="#">gi 15591148 emb AL391425.25 </a>	Human DNA sequence from clone RP...		34.2	3.9	
<a href="#">gi 22531393 emb AL359918.43 </a>	Human DNA sequence from clone RP...		34.2	3.9	
<a href="#">gi 7800095 emb AL118517.17 HSJ125M10</a>	Human DNA sequence from ...		34.2	3.9	
<a href="#">gi 6997161 gb AC023838.1 </a>	Arabidopsis thaliana chromosome III...		34.2	3.9	

<a href="#">gi 15920116 gb AC093744.2 </a>	Homo sapiens BAC clone RP11-25B14 fro	<a href="#">34.2</a>	<a href="#">3.9</a>
<a href="#">gi 3132359 dbj AP000049.1 </a>	Homo sapiens genomic DNA, chromoso...	<a href="#">34.2</a>	<a href="#">3.9</a>
<a href="#">gi 37537450 dbj BS000183.1 </a>	Pan troglodytes chromosome 22 clo...	<a href="#">34.2</a>	<a href="#">3.9</a>
<a href="#">gi 5672531 dbj AP000385.1 </a>	Arabidopsis thaliana genomic DNA, chr	<a href="#">34.2</a>	<a href="#">3.9</a>
<a href="#">gi 15883118 emb AJ338700.1 </a>	HSA338700 Homo sapiens genomic seq...	<a href="#">34.2</a>	<a href="#">3.9</a>
<a href="#">gi 7768718 dbj AP001718.1 </a>	Homo sapiens genomic DNA, chromosome	<a href="#">34.2</a>	<a href="#">3.9</a>
<a href="#">gi 4826584 dbj AP000193.1 </a>	Homo sapiens genomic DNA, chromoso...	<a href="#">34.2</a>	<a href="#">3.9</a>
<a href="#">gi 4835680 dbj AP000311.1 </a>	Homo sapiens genomic DNA, chromoso...	<a href="#">34.2</a>	<a href="#">3.9</a>
<a href="#">gi 4730851 dbj AP000117.1 </a>	Homo sapiens genomic DNA of 21q22....	<a href="#">34.2</a>	<a href="#">3.9</a>

**E**

## Alignments

Get selected sequences

Select all

Deselect all

> [gi|55645360|ref|XM\\_511474.1|](#) **U E G** PREDICTED: Pan troglodytes DNA topoisomerase II, (LOC454651), mRNA  
Length=3081

Score = 46.1 bits (23), Expect = 0.001  
Identities = 23/23 (100%), Gaps = 0/23 (0%)  
Strand=Plus/Minus

Query 1 ATTTTCCATGATCTGCTTATGAG 23  
|||||  
Sbjct 1380 ATTTTCCATGATCTGCTTATGAG 1358

> [gi|19913405|ref|NM\\_001067.2|](#) **U E G** Homo sapiens topoisomerase (DNA) II alpha 170kDa, clone IMAGE:4101949  
Length=5698

Score = 46.1 bits (23), Expect = 0.001  
Identities = 23/23 (100%), Gaps = 0/23 (0%)  
Strand=Plus/Minus

Query 1 ATTTTCCATGATCTGCTTATGAG 23  
|||||  
Sbjct 1638 ATTTTCCATGATCTGCTTATGAG 1616

> [gi|15488575|gb|BC013429.1|](#) **U E G** Homo sapiens topoisomerase (DNA) II alpha 170kDa, clone IMAGE:4101949  
Length=3076

Score = 46.1 bits (23), Expect = 0.001  
Identities = 23/23 (100%), Gaps = 0/23 (0%)  
Strand=Plus/Minus

Query 1 ATTTTCCATGATCTGCTTATGAG 23  
|||||  
Sbjct 1638 ATTTTCCATGATCTGCTTATGAG 1616

> [gi|292829|gb|J04088.1|HUMTOPII](#) **U E G** Human DNA topoisomerase II (top2) mRNA, complete cds  
Length=4792

Score = 46.1 bits (23), Expect = 0.001